

We claim:

1. The use of 2-methyl-6-solanylbenzoquinone methyltransferase in a method for identifying herbicides.
- 5 2. The use according to claim 1, wherein 2-methyl-6-solanylbenzoquinone methyltransferase is encoded by a nucleic acid sequence comprising
 - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1 or in SEQ ID NO:3; or
 - 10 ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:2 or in SEQ ID NO: 4 by back translation; or
 - 15 iii) a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4.
- 20 3. The use according to claim 2, wherein the amino acid sequence of 2-methyl-6-solanylbenzoquinone methyltransferase which is encoded by a nucleic acid sequence comprising
 - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1 or in SEQ ID NO:3; or
 - 25 ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:2 or in SEQ ID NO: 4 by back translation; or
 - 30 iii) a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4,
- 35 is truncated by at least 20 amino acids at the C terminus and by at least 20 amino acids at the N terminus.
4. The use according to any of claims 1 to 3, wherein the amino acid sequence of the truncated 2-methyl-6-solanylbenzoquinone methyltransferase is encoded by a nucleic acid sequence comprising
 - i) a nucleic acid sequence with the nucleic acid sequence shown in

SEQ ID NO:5 or in SEQ ID NO:7; or

- ii) a nucleic acid sequence which, owing to the generacy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:6 or in SEQ ID NO:8 by back translation.
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- 5. A nucleic acid sequence encoding a polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase comprising
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- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:5 or in SEQ ID NO:7; or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:6 or in SEQ ID NO: 8 by back translation; or
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- iii) SEQ ID NO:1, SEQ ID NO:3 or a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4; and is truncated by at least 20 amino acids at the C terminus and by at least 20 amino acids at the N terminus.
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- 6. A polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase encoded by a nucleic acid molecule according to claim 5.
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- 7. An expression cassette comprising
 - a) genetic control sequences in operable linkage with a nucleic acid sequence according to claim 5; or
 - b) additional functional elements; or
 - c) a combination of a) and b).
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- 8. A vector comprising an expression cassette according to claim 7.
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- 9. A nonhuman transgenic organism comprising at least one nucleic acid sequence according to claim 5, an expression cassette according to claim 7 or a vector according to claim 8, selected among bacteria, yeasts, fungi, animal or plant cells.
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- 10. A method for identifying herbicidally active substances, comprising the following

steps:

- i. bringing a polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase into contact with one or more test compounds under conditions which permit the binding of the test compound(s) to the polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase; and
 - ii. testing whether the test compound binds to the polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase; or
 - iii. detecting whether the test compound reduces or blocks the activity of the polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase of i); or
 - iv. detecting whether the test compound reduces or blocks the transcription, translation or expression of the polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase of i).
11. The method according to claim 10, wherein the polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase is encoded by a nucleic acid sequence comprising
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:5 or in SEQ ID NO:7; or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:6 or in SEQ ID NO: 8 by back translation; or
 - iii) SEQ ID NO:1, SEQ ID NO:3 or a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4; and is truncated by at least 20 amino acids at the C terminus and by at least 20 amino acids at the N terminus.
12. The method according to claim 10, wherein the amino acid sequence of 2-methyl-6-solanylbenzoquinone methyltransferase which is encoded by a nucleic acid sequence comprising
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1 or in SEQ ID NO:3; or

- ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:2 or in SEQ ID NO: 4 by back translation; or
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- iii) a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4,
- 10 is truncated by at least 20 amino acids at the C terminus and by at least 20 amino acids at the N terminus.
13. The method according to claim 10, wherein 2-methyl-6-solanylbenzoquinone methyltransferase is encoded by a nucleic acid sequence comprising
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- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:5 or in SEQ ID NO:7; or
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- ii) a nucleic acid which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:6 or in SEQ ID NO:8 by back translation.
14. A method according to claim 10, 11, 12 or 13, wherein a test compound which reduces or blocks the activity of 2-methyl-6-solanylbenzoquinone methyltransferase is selected.
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15. The method according to claim 14, which comprises
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- i. either expressing, in a transgenic organism, a 2-methyl-6-solanylbenzoquinone methyltransferase or culturing an organism which naturally comprises 2-methyl-6-solanylbenzoquinone methyltransferase;
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- ii. bringing the 2-methyl-6-solanylbenzoquinone methyltransferase of step i) in the cell digest of the transgenic or nontransgenic organism, in partially or homogeneously purified form, into contact with a test compound; and
- ii. selecting a test compound which reduces or blocks the activity of the 2-methyl-6-solanylbenzoquinone methyltransferase of step ii).
- 40 16. The method according to claim 14, which comprises the following steps:
- i. generating a transgenic organism comprising at least one nucleic acid

sequence encoding 2-methyl-6-solanylbenzoquinone methyltransferase, in which organism 2-methyl-6-solanylbenzoquinone methyltransferase is overexpressed;

- 5 ii. applying a test substance to the transgenic organism of i) and to a nontransgenic organism of the same type;
- iii. determining the growth or the viability of the transgenic and the nontransgenic organisms after application of the test substance; and
- 10 iv. selecting test substances which bring about a reduced growth or a reduced viability of the nontransgenic organism in comparison with the growth of the transgenic organism.
- 15 17. A method for identifying growth-regulatory substances, which comprises the following steps;
 - i. generation of a transgenic plant comprising a nucleic acid sequence encoding 2-methyl-6-solanylbenzoquinone methyltransferase, in which plant 2-methyl-6-solanylbenzoquinone methyltransferase is overexpressed;
 - 20 ii. applying a test substance to the transgenic plant of i) and to a nontransgenic plant of the same type;
 - iii. determining the growth or the viability of the transgenic and of the nontransgenic plants after application of the test substance; and
 - 25 iv. selecting test substances which bring about a modified growth of the nontransgenic plant in comparison with the growth of the transgenic plant.
- 30 18. The method according to any of claims 10 to 17, wherein the substances are identified in a high-throughput screening.
19. A support having one or more of the nucleic acid molecules according to claim 5, or one or more expression cassettes according to claim 7, one or more vectors according to claim 8, one or more organisms according to claim 9 or one or more (poly)peptides according to claim 6.
- 35 20. The method according to any of claims 10 to 18, wherein the substances are identified in a high-throughput screening using a support according to claim 19.
- 40 21. A herbicidally active compound identified by one of the methods according to any

of claims 10 to 16, 18 and 20.

22. A compound with growth-regulatory activity identified via the method according to any of claims 17, 18 or 20.

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23. A process for the preparation of an agrochemical composition, which comprises

a) identifying a herbicidally active compound according to claim 21 or a compound with growth-regulatory activity according to claim 22; and

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b) formulating this compound together with suitable auxiliaries to give crop protection compositions with herbicidal or growth-regulatory activity.

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24. A method for controlling undesired vegetation and/or for regulating the growth of plants, which comprises allowing at least one compound according to claim 21 or 22 or an agrochemical composition comprising a compound according to claim 21 or 22 to act on plants, their environment and/or on seeds.

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25. A method for generating nucleic acid sequences which encode 2-methyl-6-solanylbenzoquinone methyltransferase which are not inhibited by substances according to claim 21 or 22, where the nucleic acid sequence comprises

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i) a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4; or

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ii) a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4 and which is truncated by at least 20 amino acids at the C terminus and by at least 20 amino acids at the N terminus;

which comprises the following process steps:

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a) expression, in a heterologous system or in a cell-free system, of the proteins encoded by the nucleic acids of i) above;

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b) randomized or site-directed mutagenesis of the protein by modification of the nucleic acid;

c) measuring the interaction of the modified gene product with the herbicide;

- d) identification of derivatives of the protein which exhibit a lesser degree of interaction;
 - e) testing the biological activity of the protein after application of the herbicide;
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 - f) selection of the nucleic acid sequences which exhibit a modified biological activity toward the herbicide.
- 10 26. The method according to claim 25, wherein the sequences selected according to
claim 25 f) are introduced into an organism.
- 15 27. The method for generating transgenic plants which are resistant to substances
according to claim 20, which comprises overexpressing, in these plants, at least
one nucleic acid sequence which encodes 2-methyl-6-solanylbenzoquinone
methyltransferase, wherein the nucleic acid sequence comprises
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID
NO:1 or in SEQ ID NO:3; or
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 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic
code, can be derived from the amino acid sequence shown in SEQ ID NO:2
or in SEQ ID NO: 4 by back translation; or
 - 25 iii) a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which
can be derived by back translating an amino acid sequence with at least
59% identity with SEQ ID NO:4.; or
 - iv) a nucleic acid sequence of i), ii) or iii) which is truncated by at least
30 20 amino acids at the C terminus and by at least 20 amino acids at the
N terminus; or
 - v) a nucleic acid with the nucleic acid sequence shown in SEQ ID NO:5 or in
SEQ ID NO:7; or
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 - vi) a nucleic acid sequence which, owing to the degeneracy of the genetic
code, can be derived from the amino acid sequence shown in SEQ ID NO:6
or in SEQ ID NO:8 by back translation.
- 40 28. A transgenic plant, generated by a method according to claim 27.